SEQUENCE LISTING

<110> YEH, EDWARD T.H.
      GONG, LIMIN

<120> COMPOSITION AND METHODS RELATING TO SENP1 - A
      SENTRIN-SPECIFIC PROTEASE

<130> UTSH:245US1

<140> UNKNOWN
<141> 2000-07-31

<150> 60/146,774
<151> 1999-07-31

<160> 10

<170> PatentIn Ver. 2.1

<210> 1
<211> 2512
<212> DNA
<213> Human

<400> 1
acctagcgac tcttccggtg ctgtgaaggc ggttccggtt cgcggcggtt cccgggtttt 60
gcgttccgcg cccggccgga aacccccttcg catggcagcc ggttccggtt cggactttgt 120
atctttgcta aagtcagtga tgtgaaaaga cttgaaatgg atgatattgc tgataggatg 180
aggatggatg ctggagaagt gactttagtg aaccacaact ccgtattcaa aacccacctc 240
ctgccacaaa caggttttcc agaggaccag ctttcgcttt ctgaccagca gattttatct 300
tccaggcaag gacatttgga ccgatctttt acatgttcca caagaagtgc agcttataat 360
ccaagctatt actcagataa tccttcctca gacagttttc ttggctcagg cgatttaaga 420
acctttggcc agagtgcaaa tggccaatgg agaaattcta ccccatcgtc aagctcatct 480
ttacaaaaat caagaaacag ccgaagtctt tacctcgaaa cccgaaagac ctcaagtgga 540
ttatcaaaca gttttgcggg aaagtcaaac catcactgcc atgtatctgc atatgaaaaa 600
tcttttccta ttaaacctgt tccaagtcca tcttggagtg gttcatgtcg tcgaagtctt 660
ttgagcccca agaaaactca gaggcgacat gttagtacag cagaagagac agttcaagaa 720
gaagaaagag agatttacag acagctgcta cagatggtca cagggaaaca gtttactata 780
gccaaaccca ccacacattt tcctttacac ctgtctcgat gtcttagttc cagtaaaaat 840
actttgaaag actcactgtt taaaaatgga aactcttgtg catctcagat cattggctct 900
gatacttcat catctggatc tgccagcatt ttaactaacc aggaacagct gtcccacagt 960
gtatattccc tatcttctta taccccagat gttgcatttg gatccaaaga ttctggtact 1020
cttcatcatc cccatcatca ccactctgtt ccacatcagc cagataactt agcagcttca 1080
aatacacaat ctgaaggatc agactctgtg attttactga aagtgaaaga ttcccagact 1140
ccaactccca gttctacttt cttccaggca gagctgtgga tcaaagaatt aactagtgtt 1200
tatgattctc gagcacgaga aagattgcgc cagattgaag aacagaaggc attggcctta 1260
cagcttcaaa accagagatt gcaggagcgg gaacattcag tacatgattc agtagaacta 1320
catcttcgtg tacctcttga aaaggagatt cctgttactg ttgtccaaga aacacaaaaa 1380
aaaggtcata aattaactga tagtgaagat gaatttcctg aaattacaga ggaaatggag 1440
aaagaaataa agaatgtatt tcgtaatggg aatcaggatg aagttctcag tgaagcattt 1500
cgcctgacca ttacacgcaa agatattcaa actctaaacc atctgaattg gctcaatgat 1560
gagatcatca atttctacat gaatatgctg atggagcgaa gtaaagagaa gggcttgcca 1620
agtgtgcatg catttaatac cttttttcttc actaaattaa aaacggctgg ttatcaggca 1680
gtgaaacgtt ggacaaagaa agtagatgta ttttctgttg acattctttt ggtgcccatt 1740
cacctgggag tacactggtg tctagctgtt gtggacttta gaaagaagaa tattacctat 1800
tacgactcca tgggtgggat aaacaatgaa gcctgcagaa tactcttgca atacctaaag 1860

```
caagaaagca ttgacaagaa aaggaaagag tttgacacca atggctggca gctttttcagc 1920
aagaaaagcc agattcctca gcagatgaat ggaagtgact gtgggatgtt tgcctgcaaa 1980
tatgctgact gtattaccaa agacagacca atcaacttca cacagcaaca catgccatac 2040
ttccggaagc ggatggtctg ggagatcctc accgaaaac tcttgtgaag actgtctcac 2100
ttagcagacc ttgaccatgt gggggaccag ctctttgttg tctacagcca gagaccttgg 2160
aaacagctgc tcccagccct ctgctgttgt aacacccttg atcctggacc aggccctggc 2220
gagatgcatt cacaagcaca tctgcctttc cttttgtatc tcagatacta ttttttgcaaa 2280
gaaactttgg tgctgtgaaa ggggtgaggg acatccctaa gctgaagaga gagactgctt 2340
ttcacttctt cagttctgcc atcttgtttt caaagggctc cagcctcact cagtccctaa 2400
ttatgggact gagaaaagct tggaaagaat cttggtttca tataaattct tgttgttagg 2460
ccttactaag aagtaggaaa gggcatgggc aaaaggtagg gataaaaacc ac      2512


<210> 2
<211> 643
<212> PRT
<213> Human

<400> 2
Met Asp Asp Ile Ala Asp Arg Met Arg Met Asp Ala Gly Glu Val Thr
  1               5                  10                  15

Leu Val Asn His Asn Ser Val Phe Lys Thr His Leu Leu Pro Gln Thr
              20                  25                  30

Gly Phe Pro Glu Asp Gln Leu Ser Leu Ser Asp Gln Gln Ile Leu Ser
          35                  40                  45

Ser Arg Gln Gly His Leu Asp Arg Ser Phe Thr Cys Ser Thr Arg Ser
      50                  55                  60

Ala Ala Tyr Asn Pro Ser Tyr Tyr Ser Asp Asn Pro Ser Ser Asp Ser
 65                  70                  75                  80

Phe Leu Gly Ser Gly Asp Leu Arg Thr Phe Gly Gln Ser Ala Asn Gly
              85                  90                  95

Gln Trp Arg Asn Ser Thr Pro Ser Ser Ser Ser Ser Leu Gln Lys Ser
             100                 105                 110

Arg Asn Ser Arg Ser Leu Tyr Leu Glu Thr Arg Lys Thr Ser Ser Gly
          115                 120                 125

Leu Ser Asn Ser Phe Ala Gly Lys Ser Asn His His Cys His Val Ser
      130                 135                 140

Ala Tyr Glu Lys Ser Phe Pro Ile Lys Pro Val Pro Ser Pro Ser Trp
145                 150                 155                 160

Ser Gly Ser Cys Arg Arg Ser Leu Leu Ser Pro Lys Lys Thr Gln Arg
              165                 170                 175

Arg His Val Ser Thr Ala Glu Glu Thr Val Gln Glu Glu Glu Arg Glu
          180                 185                 190

Ile Tyr Arg Gln Leu Leu Gln Met Val Thr Gly Lys Gln Phe Thr Ile
          195                 200                 205
```

```
Ala Lys Pro Thr Thr His Phe Pro Leu His Leu Ser Arg Cys Leu Ser
    210             215             220
Ser Ser Lys Asn Thr Leu Lys Asp Ser Leu Phe Lys Asn Gly Asn Ser
225             230             235                 240
Cys Ala Ser Gln Ile Ile Gly Ser Asp Thr Ser Ser Ser Gly Ser Ala
            245             250                 255
Ser Ile Leu Thr Asn Gln Glu Gln Leu Ser His Ser Val Tyr Ser Leu
            260             265             270
Ser Ser Tyr Thr Pro Asp Val Ala Phe Gly Ser Lys Asp Ser Gly Thr
        275             280             285
Leu His His Pro His His His His Ser Val Pro His Gln Pro Asp Asn
    290             295             300
Leu Ala Ala Ser Asn Thr Gln Ser Glu Gly Ser Asp Ser Val Ile Leu
305             310             315             320
Leu Lys Val Lys Asp Ser Gln Thr Pro Thr Pro Ser Ser Thr Phe Phe
            325             330             335
Gln Ala Glu Leu Trp Ile Lys Glu Leu Thr Ser Val Tyr Asp Ser Arg
            340             345             350
Ala Arg Glu Arg Leu Arg Gln Ile Glu Glu Gln Lys Ala Leu Ala Leu
        355             360             365
Gln Leu Gln Asn Gln Arg Leu Gln Glu Arg Glu His Ser Val His Asp
    370             375             380
Ser Val Glu Leu His Leu Arg Val Pro Leu Glu Lys Glu Ile Pro Val
385             390             395             400
Thr Val Val Gln Glu Thr Gln Lys Lys Gly His Lys Leu Thr Asp Ser
            405             410             415
Glu Asp Glu Phe Pro Glu Ile Thr Glu Glu Met Glu Lys Glu Ile Lys
            420             425             430
Asn Val Phe Arg Asn Gly Asn Gln Asp Glu Val Leu Ser Glu Ala Phe
            435             440             445
Arg Leu Thr Ile Thr Arg Lys Asp Ile Gln Thr Leu Asn His Leu Asn
    450             455             460
Trp Leu Asn Asp Glu Ile Ile Asn Phe Tyr Met Asn Met Leu Met Glu
465             470             475             480
Arg Ser Lys Glu Lys Gly Leu Pro Ser Val His Ala Phe Asn Thr Phe
            485             490             495
Phe Phe Thr Lys Leu Lys Thr Ala Gly Tyr Gln Ala Val Lys Arg Trp
        500             505             510
```

```
Thr Lys Lys Val Asp Val Phe Ser Val Asp Ile Leu Leu Val Pro Ile
        515             520             525

His Leu Gly Val His Trp Cys Leu Ala Val Val Asp Phe Arg Lys Lys
        530             535             540

Asn Ile Thr Tyr Tyr Asp Ser Met Gly Gly Ile Asn Asn Glu Ala Cys
545             550             555             560

Arg Ile Leu Leu Gln Tyr Leu Lys Gln Glu Ser Ile Asp Lys Lys Arg
            565             570             575

Lys Glu Phe Asp Thr Asn Gly Trp Gln Leu Phe Ser Lys Lys Ser Gln
        580             585             590

Ile Pro Gln Gln Met Asn Gly Ser Asp Cys Gly Met Phe Ala Cys Lys
        595             600             605

Tyr Ala Asp Cys Ile Thr Lys Asp Arg Pro Ile Asn Phe Thr Gln Gln
    610             615             620

His Met Pro Tyr Phe Arg Lys Arg Met Val Trp Glu Ile Leu His Arg
625             630             635             640

Lys Leu Leu


<210> 3
<211> 9
<212> PRT
<213> Influenza virus

<400> 3
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
  1               5


<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   Synthetic
      Peptide

<400> 4
Arg Gly Ser His His His His
  1               5


<210> 5
<211> 28
<212> DNA
<213> Human
```

```
<400> 5
cattttaact aaccaggaac agctgtcc                                    28


<210> 6
<211> 25
<212> DNA
<213> Human

<400> 6
caagagtttt cggtggagga tctcc                                       25


<210> 7
<211> 2795
<212> DNA
<213> Human

<400> 7
accacaaagc ccatggtaac ttctgcttgt aatggaacaa ggaatgtggc cccttcagga 60
gaggtatttt cgaactcttc atcttgtgaa ctgacaggtt ctggatcctg gaacaacatg 120
ctgaaactgg gtaataaatc tcctaatgga ataagtgact atccaaagat cagagtgaca 180
gttacccgag atcagccacg cagagtcctg ccttcctttg gttttacttt gaactcagaa 240
ggctgtaata aaagaccagg tggccgtcgc catagcaaag gtaatccaga gagttcttta 300
atgtggaaac ctcaggaaca ggctgtaaca gagatgattt ctgaagagag tggcaagggt 360
ctgaggcgtc cccattgtac tgtggaggag ggtgttcaaa aagaggaaag agagaagtac 420
cgaaagttat tggaacgact taaagaaagt ggtcatggaa actctgtctg tcctgtaact 480
tcaaattatc acagttctca aagaagtcag atggacacat aaagaccaa aggctggggg 540
gaagagcaaa atcacggagt caaaacaact cagtttgttc caaaacaata tagacttgtt 600
gaaacaaggg gacctctatg ttcattgaga agtgaaaaga ggtgttcaaa ggggaaaatt 660
actgatacag agaagatggt cggaatcaga tttgaaaatg aaagtaggag gggataccaa 720
ctggagcctg acctatcaga agaagtgtcg gcccgactcc gcctgggcag tggaagcaat 780
ggcttactca ggaggaaagt gtcaataatt gagacaaagg aaaagaattg ctcaggcaaa 840
gagagggaca gaagaacgga cgatctcctt gaacttacag aggacatgga aaaggaaatc 900
agtaatgccc taggccatgg cccacaggat gaaatcctaa gtagtgcttt caaattgcga 960
attactcgag gagatattca gacattaaag aactatcact ggctcaatga tgaagtcatt 1020
aattttttaca tgaatcttct ggtggaaaga aataaaaagc aaggctatcc agcacttcat 1080
gtattcagta ctttcttcta tcctaaatta aagtctgggg gttaccaagc agtgaaacga 1140
tggaccaaag gggtaaatct ctttgaacaa gaaattattc tggtgcctat tcatcggaag 1200
gtacattgga gcctggtggt gattgaccta agaaaaaagt gtcttaaata tctggattct 1260
atgggacaaa agggccacag gatctgtgag attctccttc agtatttaca ggatgaaagt 1320
aagaccaaaa gaaatagtga tctgaatctt ttagagtgga cccatcacag catgaaacca 1380
cacgagattc ctcaacagct gaatgggagt gattgtggaa tgtttacttg taaatatgca 1440
gattatattt ctagggacaa acctatcaca tttactcagc accagatgcc tctcttccgg 1500
aagaagatgg tgtgggaaat ccttcatcag cagttgctgt gagaaaactt tgcctggtcc 1560
ctctagctgc tggtggttct ttcacagaca tttccatata cctcatgcat tgtgggttaa 1620
aaagtccctg catcacttct gttctcacag gtactgagct gtcaaaagtg catgaaggcc 1680
tctcactgta ctctagtcct gacttggggt gcagagggct gcttgcaatc ctgtttgtaa 1740
ggctgtgcct gctcagagct ttggactgtt caacccacac aagaacaaac gctaactaat 1800
attttttta agagattctt ttccctatga atgtgggaaa tgcaggattt attctgtgaa 1860
ttgtttgttt ctgtgtgttt gttcagcgta ttcattcact cactcgtttg caaacataat 1920
gggcagtggt catttactgc tgctctttta cagttagctc taaattactt gtttgaacta 1980
tttatttctg aaaggaatgt tactcaagct gccactccct gctgaagagc aggagggaac 2040
tctcactggg ggcggaagga agtggagctg gagcagtaac tgccaacatg aagctggagg 2100
gtttgggatt ttttttgttt ttgttttttt gaggctcaaa aaatgctggg agaaatgaaa 2160
atgctgtggg atagggctcc tgttgccttt cagaggaagt ctgacactac agcgttggca 2220
```

260917.1

```
cagtgccgtg aacagtggaa ctgtgcccaa gggactctga ctatccaagc atcttccgaa 2280
gagtgttgtg gtcaccttaa agagacttcc ctttctggaa atgtggtgac ttggcttagt 2340
cttcaaactg gattcatgga tttgaagtaa ctgtaaaccc taaatcttca ttttcatccc 2400
agatctggtt gagtataaac ctcagaattg taggggctgg cctgagctgt ttatttcaaa 2460
agatactatt caatttaaag ctattttttcc tcagagtttt tgttttctat atattaagtc 2520
taaattaagt tttctactca ttaagactaa catctcccca ctccatcccc actgaaattt 2580
gtggaagaaa atttagtact ggctctgag gttgccagtt atacaataat ctattttgca 2640
tatgaaagtt tgtatttaac ttttttgttc attaaaaacc ttactgatat ggttataact 2700
tcagacagtt tagagttggt cagaacatat tttgcaagat ctagtgccta gtgttgcttt 2760
tctgatgtaa taaaaggtgg tctggcagaa cctaa 2795


<210> 8
<211> 509
<212> PRT
<213> Human

<400> 8
Met Val Thr Ser Ala Cys Asn Gly Thr Arg Asn Val Ala Pro Ser Gly
 1               5                  10                  15

Glu Val Phe Ser Asn Ser Ser Ser Cys Glu Leu Thr Gly Ser Gly Ser
                20                  25                  30

Trp Asn Asn Met Leu Lys Leu Gly Asn Lys Ser Pro Asn Gly Ile Ser
            35                  40                  45

Asp Tyr Pro Lys Ile Arg Val Thr Val Thr Arg Asp Gln Pro Arg Arg
        50                  55                  60

Val Leu Pro Ser Phe Gly Phe Thr Leu Asn Ser Glu Gly Cys Asn Arg
65                  70                  75                  80

Arg Pro Gly Gly Arg Arg His Ser Lys Gly Asn Pro Glu Ser Ser Leu
                85                  90                  95

Met Trp Lys Pro Gln Glu Gln Ala Val Thr Glu Met Ile Ser Glu Glu
            100                 105                 110

Ser Gly Lys Gly Leu Arg Arg Pro His Cys Thr Val Glu Glu Gly Val
        115                 120                 125

Gln Lys Glu Glu Arg Glu Lys Tyr Arg Lys Leu Leu Glu Arg Leu Lys
    130                 135                 140

Glu Ser Gly His Gly Asn Ser Val Cys Pro Val Thr Ser Asn Tyr His
145                 150                 155                 160

Ser Ser Gln Arg Ser Gln Met Asp Thr Leu Lys Thr Lys Gly Trp Gly
                165                 170                 175

Glu Glu Gln Asn His Gly Val Lys Thr Thr Gln Phe Val Pro Lys Gln
            180                 185                 190

Tyr Arg Leu Val Glu Thr Arg Gly Pro Leu Cys Ser Leu Arg Ser Glu
        195                 200                 205
```

```
Lys Arg Cys Ser Lys Gly Lys Ile Thr Asp Thr Glu Lys Met Val Gly
    210                 215                 220

Ile Arg Phe Glu Asn Glu Ser Arg Arg Gly Tyr Gln Leu Glu Pro Asp
225                 230                 235                 240

Leu Ser Glu Glu Val Ser Ala Arg Leu Arg Leu Gly Ser Gly Ser Asn
                245                 250                 255

Gly Leu Leu Arg Arg Lys Val Ser Ile Ile Glu Thr Lys Glu Lys Asn
                260                 265                 270

Cys Ser Gly Lys Glu Arg Asp Arg Arg Thr Asp Asp Leu Leu Glu Leu
            275                 280                 285

Thr Glu Asp Met Glu Lys Glu Ile Ser Asn Ala Leu Gly His Gly Pro
    290                 295                 300

Gln Asp Glu Ile Leu Ser Ser Ala Phe Lys Leu Arg Ile Thr Arg Gly
305                 310                 315                 320

Asp Ile Gln Thr Leu Lys Asn Tyr His Trp Leu Asn Asp Glu Val Ile
                325                 330                 335

Asn Phe Tyr Met Asn Leu Leu Val Glu Arg Asn Lys Lys Gln Gly Tyr
            340                 345                 350

Pro Ala Leu His Val Phe Ser Thr Phe Phe Tyr Pro Lys Leu Lys Ser
            355                 360                 365

Gly Gly Tyr Gln Ala Val Lys Arg Trp Thr Lys Gly Val Asn Leu Phe
    370                 375                 380

Glu Gln Glu Ile Ile Leu Val Pro Ile His Arg Lys Val His Trp Ser
385                 390                 395                 400

Leu Val Val Ile Asp Leu Arg Lys Lys Cys Leu Lys Tyr Leu Asp Ser
                405                 410                 415

Met Gly Gln Lys Gly His Arg Ile Cys Glu Ile Leu Leu Gln Tyr Leu
            420                 425                 430

Gln Asp Glu Ser Lys Thr Lys Arg Asn Ser Asp Leu Asn Leu Leu Glu
            435                 440                 445

Trp Thr His His Ser Met Lys Pro His Glu Ile Pro Gln Gln Leu Asn
    450                 455                 460

Gly Ser Asp Cys Gly Met Phe Thr Cys Lys Tyr Ala Asp Tyr Ile Ser
465                 470                 475                 480

Arg Asp Lys Pro Ile Thr Phe Thr Gln His Gln Met Pro Leu Phe Arg
                485                 490                 495

Lys Lys Met Val Trp Glu Ile Leu His Gln Gln Leu Leu
                500                 505
```

260917.1

-7-

<210> 9
<211> 2206
<212> DNA
<213> Human

<400> 9
agccgccttg gggcccgtcc gcccggcttc cccgctcccg ggtactggaa gatgaaagag 60
actatacaag ggaccgggtc ctggggggcct gagcctcctg acccggcac cacttactca 120
agtcccaggc gggacggtct tcgttggccc ccaccccta agccccggct caagtccggt 180
ggtggttttg ggccagatcc tgggtctggg accacagtgc caactagacg cctccctgcc 240
ccccggccat ctttttgatgc ctcagctagt gaagaagagg aagaggaaga ggaggaagat 300
gaggaggaag tagcagcttg gaggctaccc cctaggtggg gccaactggg gcctcccag 360
cgctctcgag ctctccgacc ctctcataga aaaacctgct cacagcgccg gcgccgagcc 420
atgagagcct tccagatgct gctctactca aaaagcacct cgctgacatt ccactggaag 480
ctttgggggc gccaccgggg ccggcggcgg ggcctcgcac accccaagaa ccatctttca 540
ccccagcaag ggggtgcgac gccacaggtg ccatccccct gttgtcgttt tgactccccc 600
cgggggccac ctccacccccg gctgggtctg ctaggtgctc tcatggctga ggatgggggtg 660
agagggtctc caccagtgcc ctctgggccc cccatggagg aagatggact caggtggact 720
ccaaagtctc ctctggaccc tgactcgggc ctcctttcat gtactctgcc caacggtttt 780
gggggacaat ctgggccaga aggggagcgc agcttggcac ccctgatgc cagcatcctc 840
atcagcaatg tgtgcagcat cggggaccat gtggcccagg agctttttca gggctcagat 900
ttgggcatgg cagaagaggc agagaggcct ggggagaaag ccggccagca cagcccctg 960
cgagaggagc atgtgacctg cgtacagagc atcttggacg aattccttca aacgtatggc 1020
agcctcatac ccctcagcac tgatgaggta gtagagaagc tggaggacat tttccagcag 1080
gagttttcca ccccttccag gaagggcctg gtgttgcagc tgatccagtc ttaccagcgg 1140
atgccaggca atgccatggt gaggggcttc cgagtggctt ataagcggca cgtgctgacc 1200
atggatgact tggggacctt gtatggacag aactggctca atgaccaggt gatgaacatg 1260
tatggagacc tggtcatgga cacagtccct gaaaaggtgc atttcttcaa tagtttcttc 1320
tatgataaac tccgtaccaa gggttatgat ggggtgaaaa ggtggaccaa aaacgtggac 1380
atcttcaata aggagctact gctaatcccc atccacctgg aggtgcattg gtccctcatc 1440
tctgttgatg tgaggcgacg caccatcacc tattttgact cgcagcgtac cctaaaccgc 1500
cgctgcccta agcatattgc caagtatcta caggcagagg cggtaaagaa agaccgactg 1560
gatttccacc agggctggaa aggttacttc aaaatgaatg tggccaggca gaataatgac 1620
agtgactgtg gtgctttttgt gttgcagtac tgcaagcatc tggccctgtc tcagccattc 1680
agcttcacccc agcaggacat gcccaaactt cgtcggcaga tctacaagga gctgtgtcac 1740
tgcaaactca ctgtgtgagc ctcgtacccc agaccccaag cccataaatg ggaagggaga 1800
catgggagtc ccttcccaag aaactccagt tcctttcctc tcttgcctct tcccactcac 1860
ttccctttgg tttttcatat ttaaatgttt caatttctgt attttttttt ctttgagaga 1920
atacttgttg atttctgatg tgcagggggt ggctacagaa aagcccctttt cttcctctgt 1980
ttgcagggga gtgtggccct gtggcctggg tggagcagtc atcctcccccc ttccccgtgc 2040
agggagcagg aaatcagtgc tggggggtggt gggcggacaa taggatcact gcctgccaga 2100
tcttcaaact tttatatata tatatatata tatatatata tatataaaaa tatataaatg 2160
ccacggtcct gctctggtca ataaaggatc ctttgttgat acgtaa   2206

<210> 10
<211> 568
<212> PRT
<213> Human

<400> 10
Met Lys Glu Thr Ile Gln Gly Thr Gly Ser Trp Gly Pro Glu Pro Pro
1   5   10   15

Gly Pro Gly Thr Thr Tyr Ser Ser Pro Arg Arg Asp Gly Leu Arg Trp
                20   25   30

```
Pro Pro Pro Pro Lys Pro Arg Leu Lys Ser Gly Gly Gly Phe Gly Pro
        35              40                  45

Asp Pro Gly Ser Gly Thr Thr Val Pro Thr Arg Arg Leu Pro Ala Pro
        50              55                  60

Arg Pro Ser Phe Asp Ala Ser Ala Ser Glu Glu Glu Glu Glu Glu Glu
65              70              75                      80

Glu Glu Asp Glu Glu Glu Val Ala Ala Trp Arg Leu Pro Pro Arg Trp
                85              90                  95

Gly Gln Leu Gly Ala Ser Gln Arg Ser Arg Ala Leu Arg Pro Ser His
            100             105             110

Arg Lys Thr Cys Ser Gln Arg Arg Arg Arg Ala Met Arg Ala Phe Gln
        115             120             125

Met Leu Leu Tyr Ser Lys Ser Thr Ser Leu Thr Phe His Trp Lys Leu
    130             135             140

Trp Gly Arg His Arg Gly Arg Arg Arg Gly Leu Ala His Pro Lys Asn
145             150             155                 160

His Leu Ser Pro Gln Gln Gly Gly Ala Thr Pro Gln Val Pro Ser Pro
            165             170             175

Cys Cys Arg Phe Asp Ser Pro Arg Gly Pro Pro Pro Arg Leu Gly
        180             185             190

Leu Leu Gly Ala Leu Met Ala Glu Asp Gly Val Arg Gly Ser Pro Pro
        195             200             205

Val Pro Ser Gly Pro Pro Met Glu Glu Asp Gly Leu Arg Trp Thr Pro
    210             215             220

Lys Ser Pro Leu Asp Pro Asp Ser Gly Leu Leu Ser Cys Thr Leu Pro
225             230             235             240

Asn Gly Phe Gly Gly Gln Ser Gly Pro Glu Gly Glu Arg Ser Leu Ala
            245             250             255

Pro Pro Asp Ala Ser Ile Leu Ile Ser Asn Val Cys Ser Ile Gly Asp
        260             265             270

His Val Ala Gln Glu Leu Phe Gln Gly Ser Asp Leu Gly Met Ala Glu
        275             280             285

Glu Ala Glu Arg Pro Gly Glu Lys Ala Gly Gln His Ser Pro Leu Arg
    290             295             300

Glu Glu His Val Thr Cys Val Gln Ser Ile Leu Asp Glu Phe Leu Gln
305             310             315             320

Thr Tyr Gly Ser Leu Ile Pro Leu Ser Thr Asp Glu Val Val Glu Lys
            325             330             335
```

```
Leu Glu Asp Ile Phe Gln Gln Glu Phe Ser Thr Pro Ser Arg Lys Gly
            340                 345                 350

Leu Val Leu Gln Leu Ile Gln Ser Tyr Gln Arg Met Pro Gly Asn Ala
            355                 360                 365

Met Val Arg Gly Phe Arg Val Ala Tyr Lys Arg His Val Leu Thr Met
            370                 375                 380

Asp Asp Leu Gly Thr Leu Tyr Gly Gln Asn Trp Leu Asn Asp Gln Val
385                 390                 395                 400

Met Asn Met Tyr Gly Asp Leu Val Met Asp Thr Val Pro Glu Lys Val
                405                 410                 415

His Phe Phe Asn Ser Phe Phe Tyr Asp Lys Leu Arg Thr Lys Gly Tyr
            420                 425                 430

Asp Gly Val Lys Arg Trp Thr Lys Asn Val Asp Ile Phe Asn Lys Glu
            435                 440                 445

Leu Leu Leu Ile Pro Ile His Leu Glu Val His Trp Ser Leu Ile Ser
            450                 455                 460

Val Asp Val Arg Arg Arg Thr Ile Thr Tyr Phe Asp Ser Gln Arg Thr
465                 470                 475                 480

Leu Asn Arg Arg Cys Pro Lys His Ile Ala Lys Tyr Leu Gln Ala Glu
                485                 490                 495

Ala Val Lys Lys Asp Arg Leu Asp Phe His Gln Gly Trp Lys Gly Tyr
                500                 505                 510

Phe Lys Met Asn Val Ala Arg Gln Asn Asn Asp Ser Asp Cys Gly Ala
            515                 520                 525

Phe Val Leu Gln Tyr Cys Lys His Leu Ala Leu Ser Gln Pro Phe Ser
            530                 535                 540

Phe Thr Gln Gln Asp Met Pro Lys Leu Arg Arg Gln Ile Tyr Lys Glu
545                 550                 555                 560

Leu Cys His Cys Lys Leu Thr Val
                565
```